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Gln Val Ser Lys Thr Ser Ile Gly Trp Leu Arg Leu Leu His His Gr
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Gln Ser															
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ys Ser															
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Asn Asp Ile Leu Ala Val Ala Asp Trp Gly Gln Lys Val Ser Phe Tyr

	21	n															
Gln				_		215	5					220	)				
			Gly														
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			Gly				Sei	r Tr									
			Asn														
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305					310						315	пец	ıyı	гъ	s As	sp	Arg
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			Leu 1		Ser	Glu											
			Ile I	le i	Lys :												
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Phe s	Ser	Gly 1	4 Val L 420	05 ys (	Slu A	Arg (	Glu	Trp	41 Gl:	0 n м	et G	21,,	202	Tan	41	5 -	er
Tyr ]	Ile	Lys V	420 Val I	le G	Sly G	Sly 1	Pro	425 Pro	G1.		~~ 0		30L	430	11.	e A	.rg
Gly I	Leu	435 Lys <i>1</i>	Asn G	lv G	ln 1	le i	440	Tvc	71.	y 25.		1u (	31y 145	Leu	Le	цV	al
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Ser A																	
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Phe Cy				1 Ph 5	ne Se						l Gl						
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Gln Il	le A	la Cy	s Le	ı Gl	y Va	1 T	5 or A	:85 .sp	Thr	Ası	9 Tr	p Ar	5 g G	90 lu 1	Leu	יום.	a
Met Gl 61	u A	la Le	u Glı	ı Gl	y Le	60 u As	00 SpP	he (	Glu	Thi	c Al	- 60 a Lv	5 's 1:	vs 7	 ala	Dh	-
Ile Ar																	
625			•	63	0	J - 3		u (	<u>با</u> بدر	635		e Se	r S	er I	le	Gli	1
Glu Ar	a r	s Ly	s Arg	Gl	y Gl	u Th	r A	sn A	Asn	Asp	Le:	ı Ph	е Т.4	א נופ	1.5	640	,
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Ser Ser Gly Pro Gly Asn Ser Gln Asn Ser Phe Leu Val Gln Glu Val
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Cys Met His Ile Leu Ser Glu Glu Thr Cys Phe Gln Arg Trp Val Thr 50 55 60

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Lys Glu Met Ile Arg Ser Arg Lys Ala Val Ser Lys Leu Tyr Ala Ser
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Lys Ala His Met Asn Ser Val Leu Met Gly Met Lys Asn Gln Leu Ala
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Th	r Gl	v As	n II		~ Тъг	. 37.	. 7	- 0-	90	_,	_			95	
		,	10	U TÀI	LIYI	. Ala	a Arg	g se	r GI	y Th	r Ly	s Il	e Il	e Gl	y Lys
Va	l Hi	s (3)			ጥ ኤ			10	5				11	0	
• • •		11	.u шy.	S PILE	inr	. re	1 116	e As	p Gl	y Il	e Ar	g Va	l Al	a Th	r Gly
92	» ጥu			- m\-	. ~	_,	120	)				12	5		
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	_	195	_		~1	_	200	<b>a</b> 1	•	•	<b>61</b>	205	<b>T</b>	<b>G</b>	17. I
GIn	Asp	Leu	ser	GIn	GIn		Asp	GIY	Leu	Leu		Met	ren	cys	vaı
•	210 Val	7 J -	D	77-	7	215		Co.	710	C1-	220	Th~	T 011	Tarc	T 011
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1320

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Trp Cys 290	_				295				_	300		_		
Lys Lys				310			_		315			-	_	320
Asn His		_	325				_	330		_	_	· -	335	-
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70 Pro Ala Lys His Arg Asn Thr Ser Ala Val Leu Gly Cys Leu Ala Glu 85 Lys Leu Ala Gly Pro Ala Ser Ile Gly Leu Leu Ser Pro Gly Ile Leu 100 105 110 Glu Tyr Leu Leu Gln Cys Leu Lys Leu Gln Ser His Pro Thr Val Met 120 Leu Phe Ala Leu Ile Ala Leu Glu Lys Phe Ala Gln Thr Ser Glu Asn 135 140 Lys Leu Thr Ile Ser Glu Ser Ser Ile Ser Asp Arg Leu Val Thr Leu 150 155 Glu Ser Trp Ala Asn Asp Pro Asp Tyr Leu Lys Arg Gln Val Gly Phe 165 170 Cys Ala Gln Trp Ser Leu Asp Asn Leu Phe Leu Lys Glu Gly Arg Gln 180 185 Leu Thr Tyr Glu Lys Val Asn Leu Ser Ser Ile Arg Ala Met Leu Asn 200 Ser Asn Asp Val Ser Glu Tyr Leu Lys Ile 210 215 <210> 6083 <211> 358 <212> DNA <213> Homo sapiens <400> 6083 nnacgcgtga ggggacaggc tgagaaaaaa gaattacgac ataaaataga tgaaatggaa gaaaaagaac aggagctcca ggcaaaaata gaagctttgc aagctgataa tgatttcacc aatgaaaggc taacagcttt acaagagaag ctgatcgtcg aagggcatct aaccaaagcg gtagaagaaa caaagctttc aaaagaaaat cagacaagag caaaagaatc tgattttca gatactctga gtccaagcaa ggaaaaaagc agtgacgaca ctacagacgc ccaaatggat gagcaagacc taaatgagcc tettgecaaa gtgteeettt taaaagatga ettgeagg 358 <210> 6084 <211> 101 <212> PRT <213> Homo sapiens <400> 6084 Met Glu Glu Lys Glu Gln Glu Leu Gln Ala Lys Ile Glu Ala Leu Gln Ala Asp Asn Asp Phe Thr Asn Glu Arg Leu Thr Ala Leu Gln Glu Lys 20 25 Leu Ile Val Glu Gly His Leu Thr Lys Ala Val Glu Glu Thr Lys Leu 40 Ser Lys Glu Asn Gln Thr Arg Ala Lys Glu Ser Asp Phe Ser Asp Thr Leu Ser Pro Ser Lys Glu Lys Ser Ser Asp Asp Thr Thr Asp Ala Gln

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465				-	470	_		_		475	_	_		_	480
Glu	Ala	Asp	Met		Leu	Ser	Gly	Lys		Gln	Arg	Asn	Val	Ser	Gln
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Val	Gln	Asp	Phe	Gly	Glu	Gly	Cys	Glu	Phe	Gln	Gly	Lys	Leu	Asp	Arg
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Lys	Gln	Gly	Ile	Pro	Met	Lys	Glu	Ile	Leu	Gly	Gln	Pro	Ser	Ser	Lys
-		515				-	520					525			
Ara	Met	Asn	Tyr	Ser	Glu	Val	Pro	Tvr	Val	His	Lvs	Lvs	Ser	Ser	Thr
	530		- 4			535		•			540	•			
GI v		Ara	Pro	Hie	Tage		Aen	Glu	Cve	Glv		Ser	Phe	Tle	Gln
545	Gru	ALG	FIO	1113	550	Cys	ASII	GIU	Cys	555	Dys	Ser	FILE	116	560
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Thr	Gln	His	Gln	Arg	Val	His	Thr	Gly	Glu	Lys	Pro	Tyr	Thr	Cys	Pro
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Ser	Val	His	Ser	Glv	Glu	Arq	Pro	Phe	Lvs	Cvs	Asn	Glu	Cvs	Gly	Lvs
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7.20	C111	Tarc	Ser		Gla	Cvc	7~~	Clu		Glv	Gin	Tla	Dha		Gln
Arg	GIU	Lys	660	nis	GIII	Cys	Arg	665	Cys	GLY	GIU	116	670	FILE	GIII
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Tyr	vai		Leu	TIE	GIU	HIS		var	Leu	HIS	Met	_	GIN	Lys	ASN
	_	675					680		_	_	_	685	_		
Glu	_	Asn	Gly	Ile	Cys		Glu	Ala	Tyr	Ser	_	Asn	Leu	Thr	Val
	690					695					700		•		
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705					710					715					720
Ile	Cys	Gly	Lys	Ala	Phe	Gly	Tyr	Ser	Ser	Asp	Leu	Ile	Gln	His	Tyr
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Arq	Thr	His	Thr	Ala	Glu	Lys	Pro	Tyr	Gln	Cys	Asp	Ile	Cys	Arg	Glu
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361	770	БУЗ	Ser	птэ	GIII	775	nis	GIU	Cys	Gry	780	Gry	FIIC	1111	Leu
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	Ser	HIS	Leu	Asn		HIS	GIn	Arg	TIE		Inr	GIY	GIU	rys	
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Arg	J As	p L	eu .	Lys	Ala	Gl	1 A	sn.	T.e.i	. דם	 1		7 ~~	Al:	_	_		17	5	
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Let	1 Ly. 21	s Tì O	ır '	Trp	Cys	Gly	/ Se	er	Pro	Pro	o 1	yr	Ala	Ala	a Pr	0 G	lu	Let	ı I	Phe
Glu	ı Gl	y Li	/s (	Glu	Tvr	Δer	. 61	37	Dro	T	- T	r_ 7		220 Ile	_					
225	5	•			- 1 -	230	)	- у	-10	Lly:	5 V	aı	ASP	116	r	p S	er	Leı		
Val	. Va	l Le	eu T	ľvr	Val	Lei	, Va	7	Cve	C1.	. 7	7 ~	235	Pro	_,	_			2	40
					245			_	cys	GI	у А Э	50	Leu	Pro	Ph	e A	sp			er
Thr	Let	ı Gl	n A	Asn	Leu	Arc	Al	a i	Ara	Va 1	 . т.	.eu	Ser	Gly		~ 5	<b>L</b> _	255		
				.00						265	5					_				
			_					- 2	280					Ile	201	=				
Val	Let 290	ı As )	p F	ro	Asn	Lys	Ar 29	g 1 5	Leu	Ser	M	et	Glu	Gln		e C	ys	Lys	H	is
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D~~		T.A.	7 ~~	ري د اي	Dhe		ጥሎ፦	Dha	Dro	Dro		בוג	Hic	Gln	Gln
865	FIO	neu	чэþ	GIII	870	FIO	TILL	FIIE	FIU	875		TIG	****	0.111	880
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90

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Pro Gln Thr Leu Thr Ser Thr Leu Glu His Ile Val Gly Gln Leu Asp

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65		_			Leu 70	_				75	_				80
Phe	Asp	Asp	Thr	Pro 85	Leu	Gly	Thr	Ala	Ser 90	Leu	Ala	Gln	Val	His 95	Lys
			100	_	Gly			105			-		110		
-		115			Ser		120					125			
Val	Leu 130	Ala	Val	Lys	Gln	Leu 135	Phe	Pro	Glu	Phe	Glu 140	Phe	Met	Trp	Leu
Val 145	Asp	Glu	Ala	Lys	Lys 150	Asn	Leu	Pro	Leu	Glu 155	Leu	Asp	Phe	Leu	Asn 160
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Phe	Leu	Lys	Val 180	Pro	Arg	Ile	His	Trp 185	Asp	Leu	Ser	Thr	Glu 190	Arg	Val
		195			Val	_	200	_				205	_	_	-
Met	Glu 210	Arg	Asn	Lys	Ile	Asp 215	Val	Asn	Glu	Ile	Ser 220	Arg	His	Leu	Gly
225		_			Met 230					235					240
				245	Val				250			-		255	_
Ala	Glu	Ile	Val 260	Leu	Leu	Asp	His	Gly 265	Leu	Tyr	Gln	Met	Leu 270	Thr	Glu
		275			Tyr	_	280		_			285			
_	290				Lys	295					300	_			
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	_			405	Cys				410					415	
			420		Leu			425					430		
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1380

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				85				Ala	90					95	
			100					105					110		Thr
		115					120					125			Asp
	130					135		Gly			140				
145					150			Ile		155					160
				165				Val	170					175	_
			180					Val 185					190		
		195					200	Pro				205			
	210					215		His			220				
225					230			Gly		235					240
				245				Gln	250					255	_
			260					Asp 265					270		
		275					280	Pro				285			
	290					295		Lys			300				
305					310			Ile		315					320
				325				Gly	330					335	
			340					Val 345					350		
		355					360	Val				365			
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				405				Leu	410					415	
			420					Ser 425					430		
		435					440	Asn				445			
ser	ser	GIA	Met	Ala	Val	Ala	Gly	Met	Pro	Thr	Ala	Tyr	Asp	Leu	Ser

450 455 Ser Val Ile Ala Ser Gly Ser Ser Val Gly His Asn Asn Leu Ile Pro 470 475 Leu Ala Asn Thr Gly Ile Val Asn His Thr His Ser Arg Met Gly Ser 490 495 Ile Met Ser Thr Gly Ile Val Gln Gly Ser Ser Gly Ala Gln Gly Ser 500 510 Gly Gly Ser Thr Ser Ala His Tyr Ala Val Asn Ser Gln Phe Thr 515 520 Met Gly Gly Pro Ala Ile Ser Met Ala Ser Pro Met Ser Ile Pro Thr 535 Asn Thr Met His Tyr Gly Ser 545 <210> 6161 <211> 1489 <212> DNA <213> Homo sapiens <400> 6161 ggctgcatga tcttcagcag attcagtaca gagggaagtg agctgtggga gaggaaggag gatgggggaa atggcaagaa aaggagcacc ctgcttagaa agggaacgga gccgggtgtg gtggctcacg cctgcaatcc anacaccttg ggaggccgaa gcaaggagat cacctgagcc aaaagcagca accagcagga tgggtggaaa aaagttgctg aaggctcttc aagatcctct ctgcctgctc cttctctcac agagggacag gggagggtga tgagtcagtg gactgaatgt ccccatgggg atgaaggatg gttggggtca gggtcctaga gggagggctg gaaggaggga aggagatggc cagagaagga tgtaggacac agaggtgccg ccgtggatca ccaagaggtt caggactggc cagaggaagg agaggagatc aaggcaagca tgaggcactt gggagatgca tctgtgcctg cacacagctg aaatccccag gaaataagac gggagcaggg tgggtttctg cagecgaggt gagaccaaag tgecagetea etgecaceet cagtaaagae taaettgeee 660 ttccccacaa ctcccctccc agaagtagct tgctctcctc tgcctgccac acatcggggg gctcagggaa agctcccct ccctggacag ctagtgttcc ctaggccaag gccagtccct gcagagatga ggagctggga aatcccctcc tcccatcccg cacgtccacg cgtgccagat cctgtgctgc gggcttttca cacacagcct cttagacgct tagcctgtga ggcgggtgct 900 gttgtccttc cttcccattt tgcaactgag caaacagcct gaaagagaca aaaaccaggt agttagcatg accccaaagc cactecetgg tetacgetgt tetgcageet gageetgggg 1020

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<212> PRT

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225

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Val Tyr Leu Val Ile Glu Asp Leu Lys Gln Lys Ala Ser Glu Tyr Glu
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Leu Thr Ala Thr Leu Val Leu Glu Lys Cys Leu Gln Glu Asp Val Lys
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Lys Ala Glu Leu His Leu Ser Thr Glu Arg Ala Lys Val Asp Asn Arg
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Arg Gln Asn Met Asp Phe Leu Lys Ala Lys Ser Glu Glu Phe Arg Phe
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Gly Ile Lys Ala Ala Glu Glu Gln Leu Ser Ala Arg Gly Met Asp Ala
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•	Leu	IYL	Asp	vai		AIA	rys	GIU	FIO		GIII	Arg	ASII	ASII	_
225		•	en)	<b>~</b> 1	230	D		ml	<b>~1</b>	235	77-	<b>G3</b>	m)	<b>a</b> 1	240
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Thr		Gln	Ara	Ser	Ara		Lvs	Asp	Len	Leu		Glu	Asn	Ala	Glu
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	A 1 =	Glv	Glaz	Lare		T.e.11	Δνα	T.All	Glu		Glu	Δla	Glu	Thr	
ASP	ALG	Gry	GIY	IJУЭ	دوط	neu	AL 9	neu	GIU	1.100	GIU	AIG	014		FIO
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Leu	Arg	Lys	Leu		Glu	Ser	Cys	Lys	Asp	Leu	Ser	Leu	Leu	Asp	Val
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																				Cys	
Cys 305	Gly	Gl:	n L	/s I	ro	Thi	- G]	у	Pro	G]	lv	Glv	Pr	S O L	00	Tla	. ~1	١ ـــ	7		
His	Ala	Se	r Ly	/S A	rg	Ile	e Le	u I	Phe	Se	er	Ile	۷a	1 H	is	Asp	Ly	/s	Ser	Glu	•
Lys																					
Glu	Cys	Va]	L G1	n I	le	Leu	Ph	e A	Asn	Se	r.	Arq	Tv	r Al	la i	G] 11	3.5 זמי	9 7	·	<b>~1</b>	
Leu (	370	ASI	ı Me	E V	aı	Pro	Va	l p	ro	Ту	r	Arg	Lys	s Il	le i	Ala	Су	s A	Asp	Pro	
Glu <i>1</i> 385																					
Pro (	Cys	Thr	ту	r G	ly	Val	Pr	o L	ys	Le	u I	Lys	Arg	, [ ]]	e 1	Leu	G1	цG	3] 11	400 Arg	
His S			42	0 F	16	TIE	110	∌ F.	ys	Arg	gr N	let	Phe	As	p (	3lu			le	Phe	
Thr G	ly.	Asn	Ly	s Pl	ie '	Thr	Lys	3 A	gg	Th	r T	hr	Lvs	T.o	11 C	27	430	0	•	_	
Pro P	50	GIU	As	) Tł	ır :	Ser	Ala	G.	lu	Va]	l s	er	Arg	Al.	а 1	hr	Va]	L	eu	Asp	
Leu A 465																					
Gly P	ro (	Gly	Thi	: Se	r	3ly	Glu	Le	eu	Gly	, G	ly.	Leu	Arc	r P	ro	Tle	. T.	vc	480	
Glu P	(	JIU	500	, re	u A	ısp	Ile	11	le	Gln	V.	al '	Thr	Va]	l P	ro	Asp	) P:	ro s	Ser	
Pro T																					
Glu As	sp S	Ser	Gly	Ту	r G	ly	Met	Gl	u I	Met	Le	eu :	Fhr	Ast	ə. L	ys ·	Glv	Ţ.e	-11 C	ier	
Glu As 545	א קי	a	Arg	PY	o G	1ս 50	Glu	Ar	g 1	Pro	Vá	al (	lu	Asp	Se	er 1	His	G1	.у А	sp	
Val I																					
Tyr Al	a L	ys	Ala	Ile	e G	ly :	Ile	Se	ro	lu	Pr	o v	al	Lys	Va	1 1	Pro	ラ / Tv/	o re	er	
Lys Ph	- 2	-u	ne t	nls	יש א	ro (	iLu	GI	u I	-eu	Ph	e V	al	Val	Gl	y I	Leu	Pr	o G	lu	

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		_	660	_		_ •	_	665	_	_			670		
Phe	Gln		Asn	Tyr	Asp	Ala		Leu	Ser	Arg	Ile		116	Ala	ASN
<b></b> -	•	675	<b>~1</b>	<b>~1</b> ~	11-1	~1 m	680	7	Dha	2 0 0	1	685	Tr +	C111	C1.,
Thr	ьеи 690	Arg	GIU	GIN	var	695	Asp	Leu	Pne	ASII	Lys 700	цуѕ	ıyı	GIY	GIU
ב ו ת		C1 v	Tla	Luc	Tir		t/a l	Gln	Val	Pro	Tyr	Lvs	Ara	Tle	Lvs
705	Leu	Gry	116	цуз	710	110	Val	GIII	vai	715	- 7 -	273	••9		720
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785	- 1	•	~1	<b>.</b>	790	<b>3</b>	D	**- 3	7	795	Dwo	T	T	T 011	800
GIU	Ala	ren	GIY		Asn	Arg	Pro	vai	810	vaı	Pro	TYL	Lys	815	116
7×a	) en	Car	Dro	805	Δla	V=1	Glu	Va1		Glv	Leu	Pro	Asp		Tle
ALG	ASP	JCI	820	тэр	AIG	V (4.1	GIG	825		017			830		
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Ser	Ile	Pro	Lys		Lys	Arg	Lys	Arg		Ser	Glu	Gly	Asn		Val
				885		_	_	_	890	_	_	_		895	
Ser	Ser	Ser		Ser	Ser	Ser	Ser		ser	ser	Ser	Asn		Asp	ser
**- 1	21-	C	900	7	<b>01</b>	<b>T1</b> =	C	905	17.3	C1-	Term	Dwo	910 Mot	Tra ex-	Mot
val	ATS	ser 915	ATG	ASI	GIII	TTG	920	Leu	val	GIII	Trp	925	1-16.	TAT	HEL
Va 1	Acn		Δla	Glv	T.e.r	Aen		Gln	Len	Pro	Glv		Len	Asn	Tyr
val	930	- 7 -	AIG	SLY	Lcu	935	AGT	J_11			940				-1-
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385	-1			••- •	390	***	<b>63</b>	<b>73</b> 1	<b>.</b>	395	m\		D	23-	400
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<b>~1</b>	450	Tla	C1	C0~	T1.25	455	Sor	ת 1 ת	C0*	Thy	460	uic	ארמ	บาไ	Lou
465	гуs	TTE	GLY	Ser	Tyr 470	Leu	Ser	на	Ser	475	Arg	urs	Arg	vai	480
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Val	Ala	Gly	Val	Leu	Gly	Phe	Ala		Thr	His	Asn	Leu		Ser	Met
_	_	_	500		_	_,	_	505		_	_	~1	510	1	•••
Asn	Asp	Cys 515	Ата	GIN	Lys	ııe	ьеи 520	Pro	vai	Leu	Cys	525	Leu	Inr	vaı
Asp	Pro		Lvs	Ser	Val	Ara		Gln	Ala	Phe	Lvs		Ile	Ara	Ser
	530		-,-			535	·				540			3	••
Phe	Leu	Ser	Lys	Leu	Glu	Ser	Val	Ser	Glu	Asp	Pro	Thr	Gln	Leu	Glu
545					550					55 <b>5</b>					560
Glu	Val	Glu	Lys	_	Val	His	Ala	Ala		Ser	Pro	Gly	Met	_	Gly
77.	ת ה	ח ד ת	C 0 x	565	<b>71</b> -	~1	Two	ת ות	570	Th.	C1	นาไ	eo~	575 Sor	Lon
Ala	Ala	AIA	580	пр	MIG	GIY	пр	585	Val	1111	GIY	val	590	Ser	Leu
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625	G1	A ~~	Lare	700	630	בוע	<u>روا ب</u>	A ===	80~	635 Ser	<b>Th</b> ~	בו מ	Aen	Δ~~	640 Trp
GIU	GIU	rop	ъys	645	7 1 1 T	~TQ	GIU	vsh	650	Jer	* * * * * *	n.d	rap	655	TTD
Asp	Asp	Glu	Asp		Gly	Ser	Leu	Glu		Glu	Ala	Glu	Ser		Leu

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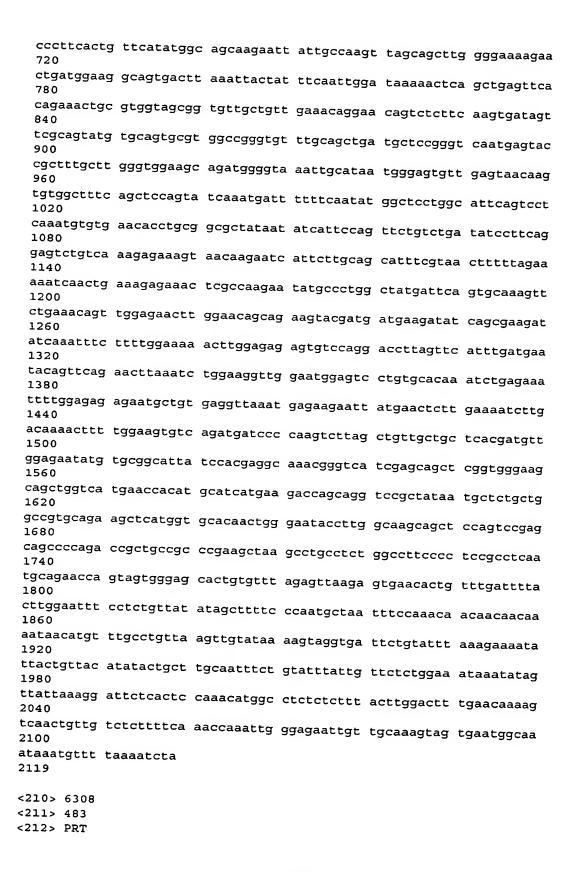
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#### What is claimed is:

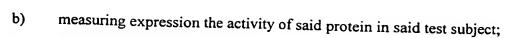
- 1. An isolated nucleic acid molecule encoding a polypeptide comprising an aminacid sequence that is at least 85% identical to a polypeptide including an amino acid sequence selected from the group consisting of SEQ ID NO:2n, wherein n is any integer 1-3161, or the complement thereof.
- 2. The isolated nucleic acid molecule of claim 1, said molecule hybridizing under stringent conditions to a nucleic acid sequence complementary to a nucleic acid molecule comprising the sequence of nucleotides selected from the group consisting of SEQ ID NO:2n-wherein n is any integer 1-3161, or the complement thereof.
- 3. The isolated nucleic acid molecule of claim 1, said molecule encoding a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ II NO: 2n, wherein n is any integer 1-3161, or an amino acid sequence comprising one or more conservative substitutions in the amino acid sequence selected from the group consisting of SI ID NO: 2n.
- 4. The isolated nucleic acid molecule of claim 1, wherein said molecule encodes: polypeptide comprising the amino acid sequence selected from the group consisting of SEQ II NO: 2n, wherein n is any integer 1-3161.
- 5. The isolated nucleic acid molecule of claim 1, wherein said molecule comprise the sequence of nucleotides selected from the group consisting of SEQ ID NO:2*n*-1, wherein *i* any integer 1-3161, or the complement thereof.
- 6. An oligonucleotide less than 100 nucleotides in length and comprising at least contiguous nucleotides selected from the group consisting of SEQ ID NO:2n-1, wherein n is a integer 1-3161, or the complement thereof.
  - 7. A vector comprising the nucleic acid molecule of claim 1.

- 8. The vector of claim 7, wherein said vector is an expression vector.
- A host cell comprising the isolated nucleic acid molecule of claim 1.
- 10. A substantially purified polypeptide comprising an amino acid sequence at least 80% identical to a polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is any integer 1-3161.
- 11. The polypeptide of claim 10, wherein said polypeptide comprises the amino acid sequence selected from the group consisting of SEQ ID NO: 2n, wherein n is any integer 1-3161.
  - 12. An antibody that selectively binds to the polypeptide of claim 10.
- 13. A pharmaceutical composition comprising a therapeutically or prophylactically effective amount of a therapeutic selected from the group consisting of:
  - a) the nucleic acid of claim 1;
  - b) the polypeptide of claim 10; and
  - c) the antibody of claim 12; and a pharmaceutically acceptable carrier.
- 14. A kit comprising in one or more containers, a therapeutically or prophylactically effective amount of the pharmaceutical composition of claim 13.
- 15. A method of producing the polypeptide of claim 10, said method comprising culturing the host cell of claim 9 under conditions in which the nucleic acid molecule is expressed.
- 16. A method of detecting the presence of the polypeptide of claim 10 in a sample, comprising contacting the sample with a compound that selectively binds to said polypeptide under conditions allowing the formation of a complex between said polypeptide and said



compound, and detecting said complex, if present, thereby identifying said polypeptide in said sample.

- 17. A method of detecting the presence of a nucleic acid molecule of claim 1 in a sample, the method comprising contacting the sample with a nucleic acid probe or primer that selectively binds to the nucleic acid molecule and determining whether the nucleic acid probe or primer bound to the nucleic acid molecule of claim 1 is present in the sample.
- 18. A method for modulating the activity of the polypeptide of claim 10, the method comprising contacting a cell sample comprising the polypeptide of claim 10 with a compound that binds to said polypeptide in an amount sufficient to modulate the activity of the polypeptid
- 19. The use of a therapeutic in the manufacture of a medicament for treating a syndrome associated with a ORFX-associated disorder, wherein said therapeutic is selected fro the group consisting of:
  - a) the nucleic acid of claim 1:
  - b) the polypeptide of claim 10; and
  - c) the antibody of claim 12.
- 20. A method for screening for a modulator of activity or of latency or predispositio to an ORFX-associated disorder, said method comprising:
  - a) contacting a test compound with the polypeptide of claim 10; and
- b) determining if said test compound binds to said polypeptide, wherein binding of said test compound to said polypeptide indicates the test compound is a modulator of activity or of latency or predisposition to an ORFX-associated disorder.
- 21. A method for screening for a modulator of activity or of latency or predisposition to an ORFX-associated disorder, said method comprising:
  - a) administering a test compound to a test subject at an increased risk ORFX-associated disorder, wherein said test subject recombinantly expresses a polypeptide encoded by the nucleotide of claim 1;



- c) measuring the activity of said protein in a control subject that recombinantly expresses said protein and is not at increased risk for an ORFX-associated disorder; and
- d) comparing expression of said protein in said test subject and said control subject, wherein a change in the activity of said protein in said test subject relative to said control subject indicates the test compound is a modulator or of latency of predisposition to an ORFX-associated disorder.
- 22. The method of claim 20, wherein said test animal is a recombinant test animal that expresses a test protein transgene or expresses said transgene under the control of a promoter at an increased level relative to a wild-type test animal, and wherein said promoter is not the native gene promoter of said transgene.
- 23. A method for determining the presence of or predisposition to a disease associated with altered levels of a polypeptide of claim 11 in a subject, the method comprising:
  - a) measuring the amount of the polypeptide in a sample from said subject; and
  - b) comparing the amount of said polypeptide in step (a) to the amount of the polypeptide present in a control sample,

wherein an alteration in the level of the polypeptide in step (a) as compared to the control sample indicates the presence of or predisposition to a disease in said subject.

- 24. The method of claim 23, wherein said subject is a human.
- 25. A method for determining the presence of or predisposition to a disease associated with altered levels the nucleic acid molecule of claim 1 in a subject, the method comprising:
  - a) measuring the amount of the nucleic acid in a sample from the mammalian subject; and
  - b) comparing the amount of said nucleic acid in step (a) to the amount of the nucleic acid present in a control sample,

wherein an alteration in the level of the nucleic acid in step (a) as compared to the corsample indicates the presence of or predisposition to said disease in said subject.

- 26. The method of claim 25, wherein said subject is a human.
- 27. A method of treating or preventing a pathological condition associated with at ORFX-associated disorder in a subject, the method comprising administering to said subject polypeptide of claim 10 in an amount sufficient to alleviate or prevent said pathological condition.
  - 28. The method of claim 27, wherein said subject is a human.
- 29. A method of treating or preventing a pathological condition associated with at ORFX-associated disorder in a subject, the method comprising administering to said subject nucleic acid molecule of claim 1 in an amount sufficient to alleviate or prevent said pathological condition.
  - 30. The method of claim 29, wherein said subject is a human.
- 31. A method of treating or preventing a pathological condition associated with ar ORFX-associated disorder in a subject, the method comprising administering to said subject antibody of claim 12 in an amount sufficient to alleviate or prevent said pathological conditions.
  - 32. The method of claim 31, wherein said subject is a human.

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# (19) World Intellectual Property Organization International Bureau





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(75) Inventors/Applicants (for US only): SHIMKETS,

(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"

(57) Abstract: The present invention provides open reading frames encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.

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	ntion) DOCUMENTS CONSIDERED TO BE RELEVANT	
Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Р,Х	M.D. ADAMS ET AL.: "The genome sequence of Drosophila melanogaster." SCIENCE, vol. 287, 24 March 2000 (2000-03-24), pages 2185-2195, XP002144875 the whole document	6
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Box I	Observations where certain claims were found unsearchable (Continua	tion of item 1 of first sheet)
This Inte	ernational Search Report has not been established in respect of certain claims under Art	icle 17(2)(a) for the following reasons:
	Claims Nos.: because they relate to subject matter not required to be searched by this Authority, name	•
	Although claims 27 to 32 are directed to a method of human/animal body, the search has been carried out effects of the compound/composition.	of treatment of the and based on the alleged
ر ــــا ا	Claims Nos.: because they relate to parts of the International Application that do not comply with the an extent that no meaningful International Search can be carried out, specifically:	prescribed requirements to such
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b	because they are dependent claims and are not drafted in accordance with the second a	and third sentences of Rule 6.4(a).
Box II C	Observations where unity of invention is lacking (Continuation of item 2	of first sheet)
This Intern	national Searching Authority found multiple inventions in this international application, a	s follows:
\$	see additional sheet	
1. A	As all required additional search fees were timely paid by the applicant, this International searchable claims.	Search Report covers all
2. As	As all searchable claims could be searched without effort justifying an additional fee, this of any additional fee.	Authority did not invite payment
3. As	s only some of the required additional search fees were timely paid by the applicant, thi overs only those claims for which fees were paid, specifically claims Nos.:	s International Search Report
163	to required additional search fees were timely paid by the applicant. Consequently, this restricted to the invention first mentioned in the claims; it is covered by claims Nos.:	International Search Report is
Remark on	The additional search fees were accompanied the payment	,

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